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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/875,520

DATE: 12/26/2001

TIME: 16:18:14

Input Set : N:\Crif3\RULE60\09875520.txt

Output Set: N:\CRF3\12262001\I875520.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Hawkins, Phillip R.

6 Murry, Lynn E.

8 (ii) TITLE OF INVENTION: HUMAN PHOSPHOLIPASE INHIBITOR

10 (iii) NUMBER OF SEQUENCES: 15

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

14 (B) STREET: 3174 Porter Drive

15 (C) CITY: Palo Alto

16 (D) STATE: CA

17 (E) COUNTRY: U.S.

18 (F) ZIP: 94304

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette

22 (B) COMPUTER: IBM Compatible

23 (C) OPERATING SYSTEM: DOS

24 (D) SOFTWARE: FastSEQ Version 1.5

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/875,520

C--> 28 (B) FILING DATE: 06-Jun-2001

30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: 09/364,790

32 (B) FILING DATE:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Luther, Barbara J.

36 (B) REGISTRATION NUMBER: 33,954

37 (C) REFERENCE/DOCKET NUMBER: PF-0059-1 US

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 415-855-0555

41 (B) TELEFAX: 415-852-0195

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 839 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: single

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: cDNA

54 (vii) IMMEDIATE SOURCE:

55 (A) LIBRARY: THP1LPB02

56 (B) CLONE: CONSENSUS

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60	NCAATGGGCC	GGCCGTGGGA	AGGGTGAATG	TGGGTCCAGA	CCCCCCCCTC	CTCAGCTTCC	60
61	TATAAAAGCT	GGGGACCAGG	TACTGCTGAT	ACACACACCA	TGAGGCTCTC	CAGGAGACCA	120
62	GAGACCTTTC	TGCTGGCCTT	TGTGTTGCTC	TGCACCCTCC	TGGGTCTTGG	GTGCCCCTA	180
63	CACTGCGAAA	TATGTACGGC	GGCGGGGAGC	AGGTGCCATG	GCCAAATGAA	GACCTGCAGC	240
64	AGTGACAAGG	ACACATGTGT	GCTCCTGGTC	GGGAAGGCTA	CTTCAAAGGG	CAAGGAGTTG	300

ENTERED

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65 GTGCACACCT ACAAGGGCTG CATCAGGTCC CAGGACTGCT ACTCCGGCGT TATATCCACC 360
66 ACCATGGGCC CCAAGGACCA CATGGTAACC AGCTCCTTCT GCTGCCAGAG CGACGGCTGC 420
67 AACAGTGCCT TTTTGTCTGT TCCCTTGACC AATCTTACTG AGAATGGCCT GATGTGCCCC 480
68 GCCTGCACTG CGAGCTTCAG GGACAAATGC ATGGGGCCCA TGACCCACTG TACTGGAAAG 540
69 GAAAACCACT GCGTCTCCTT ATCTGGACAC GTGCAGGCTG GTATTTTCAA ACCCAGATTT 600
70 GCTATGCGGG GCTGTGCTAC AGAGAGTATG TGCTTTACCA AGCCTGGTGC TGAAGTACCC 660
71 ACAGGCACCA ATGTCCTCTT CCTCCATCAT ATAGAGTGCA CTCACTCCCC CTGAAAAGCT 720
72 ATCTGAACAG AGGAAGATAA TGTAGTGTGA AGTCCCCATT TGTCTCAGC CTGTAATTCT 780
73 CCCGTGTGCC TATAAGAAG TTAATAGAGC AAAAAAAAAA AAAAAAAAAA AAACCTCGAG 839

```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: THP1LPB02

(B) CLONE: CONSENSUS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

91 Met Arg Leu Ser Arg Arg Pro Glu Thr Phe Leu Leu Ala Phe Val Leu
92 1 5 10 15
93 Leu Cys Thr Leu Leu Gly Leu Gly Cys Pro Leu His Cys Glu Ile Cys
94 20 25 30
95 Thr Ala Ala Gly Ser Arg Cys His Gly Gln Met Lys Thr Cys Ser Ser
96 35 40 45
97 Asp Lys Asp Thr Cys Val Leu Leu Val Gly Lys Ala Thr Ser Lys Gly
98 50 55 60
99 Lys Glu Leu Val His Thr Tyr Lys Gly Cys Ile Arg Ser Gln Asp Cys
100 65 70 75 80
101 Tyr Ser Gly Val Ile Ser Thr Thr Met Gly Pro Lys Asp His Met Val
102 85 90 95
103 Thr Ser Ser Phe Cys Cys Gln Ser Asp Gly Cys Asn Ser Ala Phe Leu
104 100 105 110
105 Ser Val Pro Leu Thr Asn Leu Thr Glu Asn Gly Leu Met Cys Pro Ala
106 115 120 125
107 Cys Thr Ala Ser Phe Arg Asp Lys Cys Met Gly Pro Met Thr His Cys
108 130 135 140
109 Thr Gly Lys Glu Asn His Cys Val Ser Leu Ser Gly His Val Gln Ala
110 145 150 155 160
111 Gly Ile Phe Lys Pro Arg Phe Ala Met Arg Gly Cys Ala Thr Glu Ser
112 165 170 175
113 Met Cys Phe Thr Lys Pro Gly Ala Glu Val Pro Thr Gly Thr Asn Val
114 180 185 190
115 Leu Phe Leu His His Ile Glu Cys Thr His Ser Pro
116 195 200

```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

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123         (B) TYPE: amino acid
124         (C) STRANDEDNESS: single
125         (D) TOPOLOGY: linear
127     (ii) MOLECULE TYPE: peptide
129     (vii) IMMEDIATE SOURCE:
130         (A) LIBRARY: GenBank
131         (B) CLONE: GI 501050
133     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
135 Met Lys Tyr Leu His Thr Ile Cys Leu Leu Phe Ile Phe Val Ala Arg
136 1      5      10      15
137 Gly Asn Ser Arg Ser Cys Asp Phe Cys His Asn Ile Gly Lys Asp Cys
138      20      25      30
139 Asp Gly Tyr Glu Glu Glu Cys Ser Ser Pro Glu Asp Val Cys Gly Lys
140      35      40      45
141 Val Leu Leu Glu Ile Ser Ser Ala Ser Leu Ser Val Arg Thr Val His
142      50      55      60
143 Lys Asn Cys Phe Ser Ser Ile Cys Lys Leu Gly Gln Phe Asp Val
144      65      70      75      80
145 Asn Ile Gly His His Ser Tyr Ile Arg Gly Arg Ile Asn Cys Cys Glu
146      85      90      95
147 Lys Glu Leu Cys Glu Asp Gln Pro Phe Pro Gly Leu Pro Leu Ser Lys
148      100     105     110
149 Pro Asn Gly Tyr Tyr Cys Pro Gly Ala Ile Gly Leu Phe Thr Lys Asp
150      115     120     125
151 Ser Thr Glu Tyr Glu Ala Ile Cys Lys Gly Thr Glu Thr Lys Cys Ile
152      130     135     140
153 Asn Ile Val Gly His Arg Tyr Glu Gln Phe Pro Gly Asp Ile Ser Tyr
154      145     150     155     160
155 Asn Leu Lys Gly Cys Val Ser Ser Cys Pro Leu Leu Ser Leu Ser Asn
156      165     170     175
157 Ala Thr Phe Glu Gln Asn Arg Asn Tyr Leu Glu Lys Val Glu Cys Lys
158      180     185     190
159 Asp Ala Ile Arg Leu Ala Ser Leu
160      195     200
163 (2) INFORMATION FOR SEQ ID NO: 4:
165     (i) SEQUENCE CHARACTERISTICS:
166         (A) LENGTH: 327 base pairs
167         (B) TYPE: nucleic acid
168         (C) STRANDEDNESS: single
169         (D) TOPOLOGY: linear
171     (ii) MOLECULE TYPE: cDNA
173     (vii) IMMEDIATE SOURCE:
174         (A) LIBRARY: HMC1N0T01
175         (B) CLONE: 8941
177     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
179 GGAGGCCTAG GGTAGGCAA GACCTTGAGG CAGGGGTTGA AGCCAGGGAG TGGTCAGCCA      60
180 GCACTGTCCC TGCCTGTCCC CATCCCACAG AGGGCAAGGA GTTGGTGCAC ACCTACAAGG      120
181 GCTGCATCAG GTCCCAGGAC TGCTACTCCG GCGTTATATC NACCACCATG GGCCCCAAGG      180
182 ACCACATGGT AACCAGCTCC TTCTGNTGCC AGAGCGACGG CTGCAACAGT GCCTTTTTGT      240

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183 CTGTTCCCTT GACCAATCTT ACTGAGAATG GCCTGATGTG CCCNGCTGCA CTGCGAGTTT      300
184 NAGGGNCAAA ATNCATGGGG GCCCATT                                           327
187 (2) INFORMATION FOR SEQ ID NO: 5:
189   (i) SEQUENCE CHARACTERISTICS:
190       (A) LENGTH: 324 base pairs
191       (B) TYPE: nucleic acid
192       (C) STRANDEDNESS: single
193       (D) TOPOLOGY: linear
195   (ii) MOLECULE TYPE: cDNA
197   (vii) IMMEDIATE SOURCE:
198       (A) LIBRARY: THP1LPB01
199       (B) CLONE: 10033
201   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
203 GTTGCTCTNC ACCCTCCTGG GTCTTGGGTG CCCACTACAC TGCGAAATAT GTACGGCGGC      60
204 GGGGAGCAGG TGCCATGGCC AAATGAAGAC CTGCAGCAGT GACAAGGACA CATGTGTGCT      120
205 CCTGGTCGGG AAGGCTACTT CAAAGGGCAA GGAGTTGGTG CACACCTACA AGGGCTGCAT      180
206 CAGGTCCCAG GACTGCTACT CCGGCGTTAT ATCCACCACC ATGGGCCCCA AGGACCACAT      240
207 GGTAACCAGC TCCTTCTGCT GCAGAGCGAC GGCTGCAACA GTGCCTTTTT GTCTGTTCCC      300
208 TTGACCAATC TTAGTGAGAA TGGT                                           324
211 (2) INFORMATION FOR SEQ ID NO: 6:
213   (i) SEQUENCE CHARACTERISTICS:
214       (A) LENGTH: 262 base pairs
215       (B) TYPE: nucleic acid
216       (C) STRANDEDNESS: single
217       (D) TOPOLOGY: linear
219   (ii) MOLECULE TYPE: cDNA
221   (vii) IMMEDIATE SOURCE:
222       (A) LIBRARY: THP1LPB01
223       (B) CLONE: 10644
225   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
227 GACACATGTG TNCTCCTGGT CGGGAAGGCT ACTTCAAAGG GCAAGGAGTT GGTGCACACC      60
228 TACAAGGGCT GCATCAGGTN CCAGGACTGC TACTCCGGNG TTATATCCAC CACCATGGGC      120
229 CCCAAGGACC ACATGGTAAC CAGCTCCTTC TGCTGCCAGA GCGACGGCTG CAACAGTGCC      180
230 TTTTGTCTG TTCCCTTGAC CAATNTTACT GAGAATNGNC TGATGTGCCC CGNCTGCACT      240
231 GNGAGCTTCA GGGACAAATG CT                                           262
234 (2) INFORMATION FOR SEQ ID NO: 7:
236   (i) SEQUENCE CHARACTERISTICS:
237       (A) LENGTH: 310 base pairs
238       (B) TYPE: nucleic acid
239       (C) STRANDEDNESS: single
240       (D) TOPOLOGY: linear
242   (ii) MOLECULE TYPE: cDNA
244   (vii) IMMEDIATE SOURCE:
245       (A) LIBRARY: THP1LPB01
246       (B) CLONE: 10774
248   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
250 GACACATGTG TGCTCCTGGT CGGGAAGGCT ACTTCAAAGG GCAAGGAGTT GGTGCACACC      60
251 TACAAGGGCT GCATCAGGTC CCAGGACTGC TACTCCGGNG TTATATCCAC CACCATGGGC      120
252 CCCAAGGACC ACATGGTAAC CAGCTCCTTC TGCTGCCAGA GCGACGGCTG CAACAGTGCC      180

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```

253 TTTTGTCTG TTCCCTTANC CAATCTTACT GAGAATGGCC TGATGTGCCC CGNCTGAACT 240
254 NCGAGCTTCA GGGACAAATN CATGGGNCNA TGACCCACTG TACTGGNAAG NNAAACCACT 300
255 GNGTGTCTT 310
258 (2) INFORMATION FOR SEQ ID NO: 8:
260 (i) SEQUENCE CHARACTERISTICS:
261 (A) LENGTH: 185 base pairs
262 (B) TYPE: nucleic acid
263 (C) STRANDEDNESS: single
264 (D) TOPOLOGY: linear
266 (ii) MOLECULE TYPE: cDNA
268 (vii) IMMEDIATE SOURCE:
269 (A) LIBRARY: THP1PEB01
270 (B) CLONE: 71854
272 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
274 CTCCGGCGTT ATATCCACCA CCATGGGCCC CAAGGACCAC ATGGTAACCA GTCCTTCTG 60
275 CTGCCAGAGC GACGGCTGCA ACANTGCCTT TTTNTNTGTT CCCTTGACCA ATCTTACTGA 120
276 GAATGGCCTG ATGTGCCCCG CCTGCACTGC GAGCTTCAGG GACAAATGCA TGGGGCCCAT 180
277 GACCC 185
280 (2) INFORMATION FOR SEQ ID NO: 9:
282 (i) SEQUENCE CHARACTERISTICS:
283 (A) LENGTH: 151 base pairs
284 (B) TYPE: nucleic acid
285 (C) STRANDEDNESS: single
286 (D) TOPOLOGY: linear
288 (ii) MOLECULE TYPE: cDNA
290 (vii) IMMEDIATE SOURCE:
291 (A) LIBRARY: THP1PEB01
292 (B) CLONE: 72861
294 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
296 TTTGGTGCAC ACCTACAAGG GCTGCATCAG GTCCCAGGAC TTCTACTCCG GNGTTATATC 60
297 CACCACCATG GGCCCCAAGG ACCACATGGT AACCAGCTCC TTNTGCTGCC AGAGCGACGG 120
298 CTGCAACATT GCCTTTTNT NTGTNCCCTT G 151
301 (2) INFORMATION FOR SEQ ID NO: 10:
303 (i) SEQUENCE CHARACTERISTICS:
304 (A) LENGTH: 144 base pairs
305 (B) TYPE: nucleic acid
306 (C) STRANDEDNESS: single
307 (D) TOPOLOGY: linear
309 (ii) MOLECULE TYPE: cDNA
311 (vii) IMMEDIATE SOURCE:
312 (A) LIBRARY: THP1PEB01
313 (B) CLONE: 74452
315 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
317 CAGGACTGCT ACTCCGGNGT TATATCCACC ACCATGGGCC CCAAGGACCA CATGGTAACC 60
318 AGTCCTTCT GTCGCCAGAG CNACGGCTGC AACANTGCCT TTNTGTCTGT NCCCTTGACC 120
319 AATCTNACTG AGAATNGCCT GATT 144
322 (2) INFORMATION FOR SEQ ID NO: 11:
324 (i) SEQUENCE CHARACTERISTICS:
325 (A) LENGTH: 174 base pairs

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/875,520

DATE: 12/26/2001

TIME: 16:18:16

Input Set : N:\Crf3\RULE60\09875520.txt

Output Set: N:\CRF3\12262001\I875520.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]